

SEQUENCE LISTING

<110> Gustafsson, Claes
Govindarajin, Sridhar
Minshull, Jeremy Stephen

<120> Systems and Methods for Biopolymer
Engineering

<130> 11548-02-999

<150> PCT/US04/024752

<151> 2004-07-30

<150> 60/536,862

<151> 2004-01-15

<150> 60/536,357

<151> 2004-01-14

<150> 60/491,815

<151> 2003-08-01

<160> 3

<170> FastSEQ for windows Version 4.0

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<213> Escheria coli

<220>

<223> Escheria coli Leader Peptide

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| Met | Lys | Lys | Leu | Leu | Phe | Ala | Ile | Pro | Leu | Val | Val | Pro | Phe | Tyr | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| His | Ser | Thr | Met | | | | | | | | | | | | |
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<211> 377

<212> PRT

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<220>

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<400> 2

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| Ala | Pro | Ala | Val | Glu | Gln | Arg | Ser | Glu | Ala | Ala | Pro | Leu | Ile | Glu | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Arg | Gly | Glu | Met | Val | Ala | Asn | Lys | Tyr | Ile | Val | Lys | Phe | Lys | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Ala | Leu | Ser | Ala | Leu | Asp | Ala | Ala | Met | Glu | Lys | Ile | Ser | Gly | Lys |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Pro | Asp | His | Val | Tyr | Lys | Asn | Val | Phe | Ser | Gly | Phe | Ala | Ala | Thr | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asp | Glu | Asn | Met | Val | Arg | Val | Leu | Arg | Ala | His | Pro | Asp | Val | Glu | Tyr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ile | Glu | Gln | Asp | Ala | Val | Val | Thr | Ile | Asn | Ala | Ala | Gln | Thr | Asn | Ala |
| | | | 85 | | | | | 90 | | | | | | 95 | |

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Trp | Gly | Leu | Ala | Arg | Ile | Ser | Ser | Thr | Ser | Pro | Gly | Thr | Ser | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Tyr | Tyr | Asp | Glu | Ser | Ala | Gly | Gln | Gly | Ser | Cys | Val | Tyr | Val | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asp | Thr | Gly | Ile | Glu | Ala | Ser | His | Pro | Glu | Phe | Glu | Gly | Arg | Ala | Gln |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Met | Val | Lys | Thr | Tyr | Tyr | Tyr | Ser | Ser | Arg | Asp | Gly | Asn | Gly | His | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Thr | His | Cys | Ala | Gly | Thr | Val | Gly | Ser | Arg | Thr | Tyr | Gly | Val | Ala | Lys |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Lys | Thr | Gln | Leu | Phe | Gly | Val | Lys | Val | Leu | Asp | Asp | Asn | Gly | Ser | Gly |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Gln | Tyr | Ser | Thr | Ile | Ile | Ala | Gly | Met | Asp | Phe | Val | Ala | Ser | Asp | Lys |
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| Asn | Asn | Arg | Asn | Cys | Pro | Lys | Gly | Val | Val | Ala | Ser | Leu | Ser | Leu | Gly |
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| Gly | Gly | Tyr | Ser | Ser | Ser | Val | Asn | Ser | Ala | Ala | Ala | Arg | Leu | Gln | Ser |
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| Ser | Gly | Val | Met | Val | Ala | Val | Ala | Ala | Gly | Asn | Asn | Asn | Ala | Asp | Ala |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Arg | Asn | Tyr | Ser | Pro | Ala | Ser | Glu | Pro | Ser | Val | Cys | Thr | Val | Gly | Ala |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Ser | Asp | Arg | Tyr | Asp | Arg | Arg | Ser | Ser | Phe | Ser | Asn | Tyr | Gly | Ser | Val |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Leu | Asp | Ile | Phe | Gly | Pro | Gly | Thr | Ser | Ile | Leu | Ser | Thr | Trp | Ile | Gly |
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| Gly | Ser | Thr | Arg | Ser | Ile | Ser | Gly | Thr | Ser | Met | Ala | Thr | Pro | His | Val |
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| Ala | Gly | Leu | Ala | Ala | Tyr | Leu | Met | Thr | Leu | Gly | Lys | Thr | Thr | Ala | Ala |
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<223> Artificial nucleic acid sequence encoding Tritirachium album
Limber proteinase K

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| gcaccggccg | ttgaacagcg | ttctgaagca | gctcctctga | ttgaggcacg | tggtgaaatg | 120 |
| gtagcaaac | agtacatcgt | gaagttcaag | gagggttctg | ctctgtctgc | tctggatgct | 180 |
| gctatggaaa | agatctctgg | caagcctgat | cacgtctata | agaacgtggt | cagcgggtttc | 240 |
| gcagcaactc | tggacgagaa | catggtccgt | gtactgcgtg | ctcatccaga | cgttgaatac | 300 |
| atcgaacagg | acgctgtggt | tactatcaac | gcggcacaga | ctaacgcacc | ttgggggtctg | 360 |
| gcacgtatct | cttctacttc | cccgggtacg | tctacttact | actacgacga | gtctgcccgtg | 420 |
| caaggttctt | gcgtttacgt | gacgtatcag | ggcactcgag | cttctcatcc | tgagtttgaa | 480 |
| ggcgtgtcac | aaatggtgaa | gacctactac | tactcttccc | gtgacggtaa | tggtcacggg | 540 |
| actcattgcg | cagggtactgt | tggtagccgt | acctacgggt | ttgctaagaa | aacgcaactg | 600 |
| ttcggcggtt | aagtgtctgga | cgacaacggg | tctgggtcagt | actccaccat | tatcgcgggg | 660 |
| atggatttct | tagcgagcga | taaaaacaac | cgcaactgcc | cgaaagggtg | tgtgggttct | 720 |
| ctgtctctgg | gtggttggtta | ctcctcttct | gttaacagcg | cagctgcacg | tctgcaatct | 780 |
| tccggtgtca | tggtcgcagt | agcagctggt | aacaataacg | ctgatgcacg | caactactct | 840 |
| cctgctagcg | agccttctgt | ttgcaccgtg | ggtgcactct | atcgttatga | tcgtcgttagc | 900 |

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| | | | | | | |
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| tccttcagca | actatgggttc | cgtcctggat | atcttcggcc | ctggtacttc | tatcctgtct | 960 |
| acctggattg | gcggtagcac | tcgttccatt | tccggtacga | gcatggctac | tccacatggt | 1020 |
| gctggtctgg | cagcatacct | gatgaccctg | ggtaagacca | ctgctgcatc | cgcttgctcg | 1080 |
| tacatcgcg | atactgcaaa | caaaggcgat | ctgtctaaca | tcccgttcgg | caccgttaat | 1140 |
| ctgctggcat | acaacaacta | tcaggctgtc | gaccatcatc | atcatcatca | tag | 1193 |